Basic Local Alignment Search Tool

NCBI/ BLAST/ blastp suite-2sequences/ **Formatting Results - NBR3PYEF112**

Blast 2 sequences

alignment of GenBank Prot ID 3193318 and claimed SEQ ID NO: 2

Query ID	gi|10177290|dbj|BAB10551.1|	**Subject ID**	32133
Description	unnamed protein product [Arabidopsis thaliana]	**Description**	None
		Molecule type	amino acid
Molecule type	amino acid	**Subject Length**	228
Query Length	186	**Program**	BLASTP 2.2.25+

Dot Matrix View

Plot of gi|10177290|dbj|BAB10551.1| vs 32133 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer **B** PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Links
32133	unnamed protein product	127	127	84%	1e-34	

Alignments

```
>lcl|32133 unnamed protein product
Length=228

 Score =  127 bits (319),  Expect = 1e-34, Method: Compositional matrix adjust.
 Identities = 78/167 (47%), Positives = 96/167 (58%), Gaps = 11/167 (6%)

Query  14   ACKFLRRKCMPGCIFAPYFPPEE-PHKFANVHKIFGASNVTKLLNELLPHQREDAVNSLA   72
            ACKFLRRKC+ GCIFAPYF E+     FA VHK+FGASNV+KLL+ +   H+R DAV S+
Sbjct  20   ACKFLRRKCVAGCIFAPYFDSEQGAAHFAAVHKVFGASNVSKLLHHVPEHKRPDAVVSIC   79

Query  73   YEAEARVRDPVYGCVGAISYLQRQVHRLQKELDAANADLAHYGLSTSAAGAPGNVVDLVF   132
            +EA+AR+RDP+YGCV  I  LQ+QV  LQ EL     A LA     L
Sbjct  80   FEAQARLRDPIYGCVSHIVSLQQQVVSLQTELSYLQAHLATLELPQPQPPQVPVSSSGSL   139

Query  133  QPQPLPSQQLPPLNP-VYRLSGA-SPVMN------QMPRGTGGSYGT   171
             Q L   LP ++P VY LS    PVM+      Q PR +   +G
Sbjct  140  --QALSITDLPTISPSVYDLSSIFEPVMSSTWAMQQQPRPSDHLFGV   184
```